

RAW SEQUENCE LISTING

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Application Serial Number: 10/519,943
Source: PT
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/519,943

DATE: 03/31/2006

TIME: 15:38:59

Input Set : A:\Final sequence list-12810-00140-US.txt
 Output Set: N:\CRF4\03312006\J519943.raw

3 <110> APPLICANT: Gipmans, Martijn
 4 Dahlqvist, Anders
 5 Banas, Antoni
 6 Stahl, Ulf
 7 Wiberg, Eva
 8 Lenman, Marit
 9 Ronne, Hans
 10 Stymne, Sten
 12 <120> TITLE OF INVENTION: Use of a gene for increasing the oil content in plants
 14 <130> FILE REFERENCE: 12810-00140-US
 16 <140> CURRENT APPLICATION NUMBER: US 10/519,943
 17 <141> CURRENT FILING DATE: 2004-12-29
 19 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/007084
 20 <151> PRIOR FILING DATE: 2003-07-03
 22 <150> PRIOR APPLICATION NUMBER: EP 02015344.1
 23 <151> PRIOR FILING DATE: 2002-07-10
 25 <160> NUMBER OF SEQ ID NOS: 2
 27 <170> SOFTWARE: PatentIn version 3.3
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 2439
 32 <212> TYPE: DNA
 33 <213> ORGANISM: *Saccharomyces cerevisiae*
 35 <220> FEATURE:
 36 <221> NAME/KEY: CDS
 37 <222> LOCATION: (30)..(1994)
 39 <400> SEQUENCE: 1
 40 cttgttagagg ttaactgggg agtattaca atg atg gca act ccg gct act gat 53
 41 Met Met Ala Thr Pro Ala Thr Asp
 42 1 5
 44 ctt att tcc gat aat gat aaa tat aac aag caa tgt ctt tct gat tca 101
 45 Leu Ile Ser Asp Asn Asp Lys Tyr Asn Lys Gln Cys Leu Ser Asp Ser
 46 10 15 20
 48 agt gat agt ggt agt gat gta agc ttt tcc gta aat gaa agc gaa 149
 49 Ser Asp Ser Gly Ser Asp Val Ser Phe Phe Ser Val Asn Glu Ser Glu
 50 25 30 35 40
 52 ggt gaa ttg gat aca atg gag aaa gtg gat acc ttg att gga ggt gca 197
 53 Gly Glu Leu Asp Thr Met Glu Lys Val Asp Thr Leu Ile Gly Gly Ala
 54 45 50 55
 56 aga gtt ata agc aat aaa gta gaa aaa gac agc gat agt gaa caa agg 245
 57 Arg Val Ile Ser Asn Lys Val Glu Lys Asp Ser Asp Ser Glu Gln Arg
 58 60 65 70
 60 gga aga aag aag gaa aca act ggg ccc aat aac tat cat aat tta gaa 293
 61 Gly Arg Lys Lys Glu Thr Thr Gly Pro Asn Asn Tyr His Asn Leu Glu

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62	75	80	85	
64	gag aag caa gcg agt gcc att tct ctt gac gct gat gat gaa gat ctc			341
65	Glu Lys Gln Ala Ser Ala Ile Ser Leu Asp Ala Asp Asp Glu Asp Leu			
66	90	95	100	
68	gat gaa att att tct tat tcg cat gac ggg aac tat gac agc tct cat			389
69	Asp Glu Ile Ile Ser Tyr Ser His Asp Gly Asn Tyr Asp Ser Ser His			
70	105	110	115	120
72	aaa act ttc tcc ttt tcc cca ttt ggt aat aca aat ttc cga tca			437
73	Lys Thr Phe Ser Phe Ser Leu Pro Phe Gly Asn Thr Asn Phe Arg Ser			
74	125	130	135	
76	agt tca cca tta gcc ata att aaa act gtg ctt ccc aag act cca gat			485
77	Ser Ser Pro Leu Ala Ile Ile Lys Thr Val Leu Pro Lys Thr Pro Asp			
78	140	145	150	
80	gag ttc atc aaa aag aat cta aga aag aat gag atc aag caa aaa ctg			533
81	Glu Phe Ile Lys Lys Asn Leu Arg Lys Asn Glu Ile Lys Gln Lys Leu			
82	155	160	165	
84	aaa aaa tca acc tcc att tct tcc ttg gaa gag ata gaa tta ttt aaa			581
85	Lys Lys Ser Thr Ser Ile Ser Ser Leu Glu Glu Ile Glu Leu Phe Lys			
86	170	175	180	
88	tac gaa agg ggc att gat aat tca agg tta agg gct gtt aaa gaa tct			629
89	Tyr Glu Arg Gly Ile Asp Asn Ser Arg Leu Arg Ala Val Lys Glu Ser			
90	185	190	195	200
92	ttg gaa atg gat gcc ttg aag aac tcc att aag caa ata aca gca gac			677
93	Leu Glu Met Asp Ala Leu Lys Asn Ser Ile Lys Gln Ile Thr Ala Asp			
94	205	210	215	
96	cca ttc gac aaa act cat gac gga tat tac cgt tcg cgt tta gaa tct			725
97	Pro Phe Asp Lys Thr His Asp Gly Tyr Tyr Arg Ser Arg Leu Glu Ser			
98	220	225	230	
100	ata tgg aat gaa ttg gaa gga gat gtc gtt ata atg ggt tat cga			773
101	Ile Trp Asn Glu Leu Glu Gly Asp Val Val Ile Met Gly Gly Tyr Arg			
102	235	240	245	
104	ggt agt gtg cta agg gat gct act act cat aag cga att tgg atc cca			821
105	Gly Ser Val Leu Arg Asp Ala Thr Thr His Lys Arg Ile Trp Ile Pro			
106	250	255	260	
108	tta aag gca ggt ttg aat atg acg aaa gtc gat tta ttg atc gga cct			869
109	Leu Lys Ala Gly Leu Asn Met Thr Lys Val Asp Leu Leu Ile Gly Pro			
110	265	270	275	280
112	aat gac gaa gat gaa ctt aaa act cag aag gag att gtc cct gat gga			917
113	Asn Asp Glu Asp Glu Leu Lys Thr Gln Lys Glu Ile Val Pro Asp Gly			
114	285	290	295	
116	atg cta aca cat ata ggg cct gtt gat atc tct aag agg ttg ata aag			965
117	Met Leu Thr His Ile Gly Pro Val Asp Ile Ser Lys Arg Leu Ile Lys			
118	300	305	310	
120	agg cta gac gca aat cct aat tta aat gtt cag cag ttt ggc tat gat			1013
121	Arg Leu Asp Ala Asn Pro Asn Leu Asn Val Gln Gln Phe Gly Tyr Asp			
122	315	320	325	
124	tgg aga tta tcc ttg gac ata tct gcc aag cat tta acg act aaa cta			1061
125	Trp Arg Leu Ser Leu Asp Ile Ser Ala Lys His Leu Thr Thr Lys Leu			
126	330	335	340	

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128	gag	gaa	att	tac	aat	aag	caa	aaa	aat	aag	gga	ata	tac	atc	att	1109	
129	Glu	Glu	Ile	Tyr	Asn	Lys	Gln	Lys	Asn	Lys	Lys	Gly	Ile	Tyr	Ile	Ile	
130	345				350					355					360		
132	gcc	cat	tca	atg	ggc	gga	ttg	gtc	gca	cat	aaa	gtg	ttg	caa	gac	tgt	1157
133	Ala	His	Ser	Met	Gly	Gly	Leu	Val	Ala	His	Lys	Val	Leu	Gln	Asp	Cys	
134				365					370			375					
136	act	cat	ttg	ata	aga	ggt	att	att	tac	gtg	ggt	tcc	cca	agc	caa	tgt	1205
137	Thr	His	Leu	Ile	Arg	Gly	Ile	Ile	Tyr	Val	Gly	Ser	Pro	Ser	Gln	Cys	
138				380					385			390					
140	cca	aat	att	tta	ggt	cct	att	agg	ttt	gga	gat	gat	gtg	atg	tgg	aat	1253
141	Pro	Asn	Ile	Leu	Gly	Pro	Ile	Arg	Phe	Gly	Asp	Asp	Val	Met	Trp	Asn	
142				395					400			405					
144	aaa	cta	ttt	tca	cta	aga	acc	aac	ttt	ttt	atg	aga	agt	agt	ttc	tat	1301
145	Lys	Leu	Phe	Ser	Leu	Arg	Thr	Asn	Phe	Phe	Met	Arg	Ser	Ser	Phe	Tyr	
146				410					415			420					
148	ttt	cta	ccg	tta	gat	ggt	aga	tgt	ttt	gtt	gac	aaa	att	acc	tta	gag	1349
149	Phe	Leu	Pro	Leu	Asp	Gly	Arg	Cys	Phe	Val	Asp	Lys	Ile	Thr	Leu	Glu	
150	425				430					435			440				
152	agg	tat	gat	ttc	gat	ttt	ttt	gat	aca	gat	gtt	tgg	aaa	acc	ctt	ggc	1397
153	Arg	Tyr	Asp	Phe	Asp	Phe	Phe	Asp	Thr	Asp	Val	Trp	Lys	Thr	Leu	Gly	
154				445					450			455					
156	ttg	tca	cct	ctc	gtc	aat	gag	aaa	aga	gag	gaa	tca	gct	cac	gaa	aaa	1445
157	Leu	Ser	Pro	Leu	Val	Asn	Glu	Lys	Arg	Glu	Glu	Ser	Ala	His	Glu	Lys	
158				460					465			470					
160	tca	aaa	tta	tta	cca	agg	aaa	acg	aaa	tca	gcg	ctt	tcg	ctt	aaa	gct	1493
161	Ser	Lys	Leu	Leu	Pro	Arg	Lys	Thr	Lys	Ser	Ala	Ile	Ser	Leu	Lys	Ala	
162				475					480			485					
164	acc	cta	aac	gca	act	acc	aag	ttt	gtc	cta	aat	gca	cct	gtt	gtt	agg	1541
165	Thr	Leu	Asn	Ala	Thr	Thr	Lys	Phe	Val	Leu	Asn	Ala	Pro	Val	Val	Arg	
166				490					495			500					
168	aat	gta	gcc	ggc	aat	aat	aaa	cag	gta	cca	agg	gat	gtg	cct	ttc	gat	1589
169	Asn	Val	Ala	Gly	Asn	Asn	Lys	Gln	Val	Pro	Arg	Asp	Val	Pro	Phe	Asp	
170	505				510					515			520				
172	gaa	gtc	ttc	cat	aca	tct	tat	gaa	gat	agc	tgt	gaa	tat	tta	gcg	aga	1637
173	Glu	Val	Phe	His	Thr	Ser	Tyr	Glu	Asp	Ser	Cys	Glu	Tyr	Leu	Ala	Arg	
174				525					530			535					
176	act	tta	aaa	cgt	aca	aag	aat	tat	ttg	gat	agc	tta	gat	tac	gac	ccg	1685
177	Thr	Leu	Lys	Arg	Thr	Lys	Asn	Tyr	Leu	Asp	Ser	Leu	Asp	Tyr	Asp	Pro	
178				540					545			550					
180	aac	aaa	gaa	tat	cct	cca	ttg	gcc	atg	gtt	tac	ggt	aac	aag	gtt	ccc	1733
181	Asn	Lys	Glu	Tyr	Pro	Pro	Leu	Ala	Met	Val	Tyr	Gly	Asn	Lys	Val	Pro	
182				555					560			565					
184	act	gtt	aga	ggt	gct	aaa	gtg	aac	ggt	ata	caa	gat	ata	aaa	gat	ggg	1781
185	Thr	Val	Arg	Gly	Ala	Lys	Val	Asn	Gly	Ile	Gln	Asp	Ile	Lys	Asp	Gly	
186				570					575			580					
188	aat	tat	gaa	gat	ttt	tac	tat	ggt	ccg	ggc	gac	ggt	gtt	gtt	cac	cat	1829
189	Asn	Tyr	Glu	Asp	Phe	Tyr	Tyr	Gly	Pro	Gly	Asp	Gly	Val	Val	His	His	
190				585					590			595			600		
192	aaa	tgg	tta	ttg	cct	gaa	cag	aga	ggc	ttt	cca	gtt	gtt	tgt	aaa	atc	1877

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193 Lys Trp Leu Leu Pro Glu Gln Arg Gly Phe Pro Val Val Cys Lys Ile
194 605 610 615
196 gcc agt tct tca ggt cat gtt agc tta atg acg gat ttg aaa tca atg 1925
197 Ala Ser Ser Ser Gly His Val Ser Leu Met Thr Asp Leu Lys Ser Met
198 620 625 630
200 gca aaa gca ttc ata tct atc gtc gac agc gaa aaa gaa gga aga aga 1973
201 Ala Lys Ala Phe Ile Ser Ile Val Asp Ser Glu Lys Glu Gly Arg Arg
202 635 640 645
204 tct cga aca cga act tct tca tgaaaggctt tttattcctt tgtttactat 2024
205 Ser Arg Thr Arg Thr Ser Ser
206 650 655
208 tcataatctgc attttctttt ttacaaaaat tccgcattgtc aaaaaaaaaatc tggcaacgca 2084
210 cccgcaataa aaataaataa tattttttta tcttttagttg ccttaaataact atttatttcg 2144
212 tcaattttac aacctctttt atatacacca ttgcatttcc cacgaagtaa aataataatt 2204
214 ctataaaacag atttatctga tatgctcaat ttcccttccc attttcatta ttgtccttct 2264
216 tgctcttcctt cgatgtcaaa attaaccccttc agccataaagc tgcatgcgc acattgggtt 2324
218 aataattgtt aaccagaatg actccgttcc atagcgtcta cattatcaat gcattcatct 2384
220 aacaaaactct cactaaaatg aaaaccacca acaaattgac agcgaggaca attca 2439
223 <210> SEQ ID NO: 2
224 <211> LENGTH: 655
225 <212> TYPE: PRT
226 <213> ORGANISM: Saccharomyces cerevisiae
228 <400> SEQUENCE: 2
229 Met Met Ala Thr Pro Ala Thr Asp Leu Ile Ser Asp Asn Asp Lys Tyr
230 1 5 10 15
232 Asn Lys Gln Cys Leu Ser Asp Ser Ser Asp Ser Gly Ser Asp Val Ser
233 20 25 30
235 Phe Phe Ser Val Asn Glu Ser Glu Gly Glu Leu Asp Thr Met Glu Lys
236 35 40 45
238 Val Asp Thr Leu Ile Gly Gly Ala Arg Val Ile Ser Asn Lys Val Glu
239 50 55 60
241 Lys Asp Ser Asp Ser Glu Gln Arg Gly Arg Lys Lys Glu Thr Thr Gly
242 65 70 75 80
244 Pro Asn Asn Tyr His Asn Leu Glu Glu Lys Gln Ala Ser Ala Ile Ser
245 85 90 95
247 Leu Asp Ala Asp Asp Glu Asp Leu Asp Glu Ile Ile Ser Tyr Ser His
248 100 105 110
250 Asp Gly Asn Tyr Asp Ser Ser His Lys Thr Phe Ser Phe Ser Leu Pro
251 115 120 125
253 Phe Gly Asn Thr Asn Phe Arg Ser Ser Ser Pro Leu Ala Ile Ile Lys
254 130 135 140
256 Thr Val Leu Pro Lys Thr Pro Asp Glu Phe Ile Lys Lys Asn Leu Arg
257 145 150 155 160
259 Lys Asn Glu Ile Lys Gln Lys Leu Lys Lys Ser Thr Ser Ile Ser Ser
260 165 170 175
262 Leu Glu Glu Ile Glu Leu Phe Lys Tyr Glu Arg Gly Ile Asp Asn Ser
263 180 185 190
265 Arg Leu Arg Ala Val Lys Glu Ser Leu Glu Met Asp Ala Leu Lys Asn
266 195 200 205

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268 Ser Ile Lys Gln Ile Thr Ala Asp Pro Phe Asp Lys Thr His Asp Gly
269 210 215 220
271 Tyr Tyr Arg Ser Arg Leu Glu Ser Ile Trp Asn Glu Leu Glu Gly Asp
272 225 230 235 240
274 Val Val Ile Met Gly Gly Tyr Arg Gly Ser Val Leu Arg Asp Ala Thr
275 245 250 255
277 Thr His Lys Arg Ile Trp Ile Pro Leu Lys Ala Gly Leu Asn Met Thr
278 260 265 270
280 Lys Val Asp Leu Leu Ile Gly Pro Asn Asp Glu Asp Glu Leu Lys Thr
281 275 280 285
283 Gln Lys Glu Ile Val Pro Asp Gly Met Leu Thr His Ile Gly Pro Val
284 290 295 300
286 Asp Ile Ser Lys Arg Leu Ile Lys Arg Leu Asp Ala Asn Pro Asn Leu
287 305 310 315 320
289 Asn Val Gln Gln Phe Gly Tyr Asp Trp Arg Leu Ser Leu Asp Ile Ser
290 325 330 335
292 Ala Lys His Leu Thr Thr Lys Leu Glu Glu Ile Tyr Asn Lys Gln Lys
293 340 345 350
295 Asn Lys Lys Gly Ile Tyr Ile Ile Ala His Ser Met Gly Gly Leu Val
296 355 360 365
298 Ala His Lys Val Leu Gln Asp Cys Thr His Leu Ile Arg Gly Ile Ile
299 370 375 380
301 Tyr Val Gly Ser Pro Ser Gln Cys Pro Asn Ile Leu Gly Pro Ile Arg
302 385 390 395 400
304 Phe Gly Asp Asp Val Met Trp Asn Lys Leu Phe Ser Leu Arg Thr Asn
305 405 410 415
307 Phe Phe Met Arg Ser Ser Phe Tyr Phe Leu Pro Leu Asp Gly Arg Cys
308 420 425 430
310 Phe Val Asp Lys Ile Thr Leu Glu Arg Tyr Asp Phe Asp Phe Phe Asp
311 435 440 445
313 Thr Asp Val Trp Lys Thr Leu Gly Leu Ser Pro Leu Val Asn Glu Lys
314 450 455 460
316 Arg Glu Glu Ser Ala His Glu Lys Ser Lys Leu Leu Pro Arg Lys Thr
317 465 470 475 480
319 Lys Ser Ala Leu Ser Leu Lys Ala Thr Leu Asn Ala Thr Thr Lys Phe
320 485 490 495
322 Val Leu Asn Ala Pro Val Val Arg Asn Val Ala Gly Asn Asn Lys Gln
323 500 505 510
325 Val Pro Arg Asp Val Pro Phe Asp Glu Val Phe His Thr Ser Tyr Glu
326 515 520 525
328 Asp Ser Cys Glu Tyr Leu Ala Arg Thr Leu Lys Arg Thr Lys Asn Tyr
329 530 535 540
331 Leu Asp Ser Leu Asp Tyr Asp Pro Asn Lys Glu Tyr Pro Pro Leu Ala
332 545 550 555 560
334 Met Val Tyr Gly Asn Lys Val Pro Thr Val Arg Gly Ala Lys Val Asn
335 565 570 575
337 Gly Ile Gln Asp Ile Lys Asp Gly Asn Tyr Glu Asp Phe Tyr Tyr Gly
338 580 585 590
340 Pro Gly Asp Gly Val Val His His Lys Trp Leu Leu Pro Glu Gln Arg

VERIFICATION SUMMARY

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